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SEQUENCE LISTING

<110> Spiegelman, Bruce
Yoon, Cliff

<120> Methods and Compositions for Modulating Gluconeogenesis
Using PGC-1

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<151> 2001-02-05

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<170> PatentIn Ver. 2.0

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Arg Tyr Asp Ser Tyr Glu Glu Tyr Gln His Glu Arg Leu Lys Arg Glu	
635 640 645	

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gaa tat cgc aga gag tat gag aag cga gag tct gag agg gcc aag caa 2080
 Glu Tyr Arg Arg Glu Tyr Glu Lys Arg Glu Ser Glu Arg Ala Lys Gln
 650 655 660

agg gag agg cag agg cag aag gca att gaa gag cgc cgt gtg att tat 2128
 Arg Glu Arg Gln Arg Gln Lys Ala Ile Glu Glu Arg Arg Val Ile Tyr
 665 670 675 680

gtc ggt aaa atc aga cct gac aca aca cgg aca gaa ctg agg gac cgt 2176
 Val Gly Lys Ile Arg Pro Asp Thr Thr Arg Thr Glu Leu Arg Asp Arg
 685 690 695

ttt gaa gtt ttt ggt gaa att gag gag tgc aca gta aat ctg cgg gat 2224
 Phe Glu Val Phe Gly Glu Ile Glu Glu Cys Thr Val Asn Leu Arg Asp
 700 705 710

gat gga gac agc tat ggt ttc att acc tac cgt tat acc tgt gat gct 2272
 Asp Gly Asp Ser Tyr Gly Phe Ile Thr Tyr Arg Tyr Thr Cys Asp Ala
 715 720 725

ttt gct gct ctt gaa aat gga tac act ttg cgc agg tca aac gaa act 2320
 Phe Ala Ala Leu Glu Asn Gly Tyr Thr Leu Arg Arg Ser Asn Glu Thr
 730 735 740

gac ttt gag ctg tac ttt tgt gga cgc aag caa ttt ttc aag tct aac 2368
 Asp Phe Glu Leu Tyr Phe Cys Gly Arg Lys Phe Phe Lys Ser Asn
 745 750 755 760

tat gca gac cta gat tca aac tca gat gac ttt gac cct gct tcc acc 2416
 Tyr Ala Asp Leu Asp Ser Asn Ser Asp Asp Phe Asp Pro Ala Ser Thr
 765 770 775

aag agc aag tat gac tct ctg gat ttt gat agt tta ctg aaa gaa gct 2464
 Lys Ser Lys Tyr Asp Ser Leu Asp Phe Asp Ser Leu Leu Lys Glu Ala
 780 785 790

cag aga agc ttg cgc agg taacatgttc cctagctgag gatgacagag 2512
 Gln Arg Ser Leu Arg Arg
 795

ggatggcgaa tacctcatgg gacagcgcgt ccttccctaa agactattgc aagtcatact 2572

taggaatttc tctacttta cactctctgt acaaaaacaa aacaaaacaa caacaataca 2632

acaagaacaa caacaacaat aacaacaatg gtttacatga acacagctgc tgaagaggca 2692

agagacagaa tgatatccag taagcacatg tttattcatg ggtgtcagct ttgcttttcc 2752

tggagtctct tggatgatgga gtgtgcgtgt gtgcatgtat gtgtgtgtgt atgtatgtgt 2812

gtggtgtgtg tgcttgggtt aggggaagta tgtgtgggta catgtgagga ctgggggcac 2872

ctgaccagaa tgcgcaaggg caaaccattt caaatggcag cagttccatg aagacacact 2932

taaaacctag aacttcaaaa tgttcgtatt ctattcaaaa ggaaaaatat atatatatat 2992

atatatatat aaattaaaaa aaaaaaaaaa a 3023

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<210> 5
 <211> 798
 <212> PRT
 <213> Homo sapiens

<400> 5

Met	Ala	Trp	Asp	Met	Cys	Asn	Gln	Asp	Ser	Glu	Ser	Val	Trp	Ser	Asp
1				5					10					15	
Ile	Glu	Cys	Ala	Ala	Leu	Val	Gly	Glu	Asp	Gln	Pro	Leu	Cys	Pro	Asp
			20					25					30		
Leu	Pro	Glu	Leu	Asp	Leu	Ser	Glu	Leu	Asp	Val	Asn	Asp	Leu	Asp	Thr
		35					40					45			
Asp	Ser	Phe	Leu	Gly	Gly	Leu	Lys	Trp	Cys	Ser	Asp	Gln	Ser	Glu	Ile
	50					55					60				
Ile	Ser	Asn	Gln	Tyr	Asn	Asn	Glu	Pro	Ser	Asn	Ile	Phe	Glu	Lys	Ile
	65				70					75					80
Asp	Glu	Glu	Asn	Glu	Ala	Asn	Leu	Leu	Ala	Val	Leu	Thr	Glu	Thr	Leu
				85					90					95	
Asp	Ser	Leu	Pro	Val	Asp	Glu	Asp	Gly	Leu	Pro	Ser	Phe	Asp	Ala	Leu
			100					105					110		
Thr	Asp	Gly	Asp	Val	Thr	Thr	Asp	Asn	Glu	Ala	Ser	Pro	Ser	Ser	Met
		115					120						125		
Pro	Asp	Gly	Thr	Pro	Pro	Pro	Gln	Glu	Ala	Glu	Glu	Pro	Ser	Leu	Leu
	130					135						140			
Lys	Lys	Leu	Leu	Leu	Ala	Pro	Ala	Asn	Thr	Gln	Leu	Ser	Tyr	Asn	Glu
145					150					155					160
Cys	Ser	Gly	Leu	Ser	Thr	Gln	Asn	His	Ala	Asn	His	Asn	His	Arg	Ile
				165					170					175	
Arg	Thr	Asn	Pro	Ala	Ile	Val	Lys	Thr	Glu	Asn	Ser	Trp	Ser	Asn	Lys
			180					185						190	
Ala	Lys	Ser	Ile	Cys	Gln	Gln	Gln	Lys	Pro	Gln	Arg	Arg	Pro	Cys	Ser
			195				200					205			
Glu	Leu	Leu	Lys	Tyr	Leu	Thr	Thr	Asn	Asp	Asp	Pro	Pro	His	Thr	Lys
	210					215					220				
Pro	Thr	Glu	Asn	Arg	Asn	Ser	Ser	Arg	Asp	Lys	Cys	Thr	Ser	Lys	Lys
225					230					235				240	
Lys	Ser	His	Thr	Gln	Ser	Gln	Ser	Gln	His	Leu	Gln	Ala	Lys	Pro	Thr
				245				250						255	
Thr	Leu	Ser	Leu	Pro	Leu	Thr	Pro	Glu	Ser	Pro	Asn	Asp	Pro	Lys	Gly
			260					265					270		
Ser	Pro	Phe	Glu	Asn	Lys	Thr	Ile	Glu	Arg	Thr	Leu	Ser	Val	Glu	Leu
			275				280						285		

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Ser Gly Thr Ala Gly Leu Thr Pro Pro Thr Thr Pro Pro His Lys Ala
 290 295 300
 Asn Gln Asp Asn Pro Phe Arg Ala Ser Pro Lys Leu Lys Ser Ser Cys
 305 310 315 320
 Lys Thr Val Val Pro Pro Pro Ser Lys Lys Pro Arg Tyr Ser Glu Ser
 325 330 335
 Ser Gly Thr Gln Gly Asn Asn Ser Thr Lys Lys Gly Pro Glu Gln Ser
 340 345 350
 Glu Leu Tyr Ala Gln Leu Ser Lys Ser Ser Val Leu Thr Gly Gly His
 355 360 365
 Glu Glu Arg Lys Thr Lys Arg Pro Ser Leu Arg Leu Phe Gly Asp His
 370 375 380
 Asp Tyr Cys Gln Ser Ile Asn Ser Lys Thr Glu Ile Leu Ile Asn Ile
 385 390 395 400
 Ser Gln Glu Leu Gln Asp Ser Arg Gln Leu Glu Asn Lys Asp Val Ser
 405 410 415
 Ser Asp Trp Gln Gly Gln Ile Cys Ser Ser Thr Asp Ser Asp Gln Cys
 420 425 430
 Tyr Leu Arg Glu Thr Leu Glu Ala Ser Lys Gln Val Ser Pro Cys Ser
 435 440 445
 Thr Arg Lys Gln Leu Gln Asp Gln Glu Ile Arg Ala Glu Leu Asn Lys
 450 455 460
 His Phe Gly His Pro Ser Gln Ala Val Phe Asp Asp Glu Ala Asp Lys
 465 470 475 480
 Thr Gly Glu Leu Arg Asp Ser Asp Phe Ser Asn Glu Gln Phe Ser Lys
 485 490 495
 Leu Pro Met Phe Ile Asn Ser Gly Leu Ala Met Asp Gly Leu Phe Asp
 500 505 510
 Asp Ser Glu Asp Lys Ser Asp Lys Leu Ser Tyr Pro Trp Asp Gly Thr
 515 520 525
 Gln Ser Tyr Ser Leu Phe Asn Val Ser Pro Ser Cys Ser Ser Phe Asn
 530 535 540
 Ser Pro Cys Arg Asp Ser Val Ser Pro Pro Lys Ser Leu Phe Ser Gln
 545 550 555 560
 Arg Pro Gln Arg Met Arg Ser Arg Ser Arg Ser Phe Ser Arg His Arg
 565 570 575
 Ser Cys Ser Arg Ser Pro Tyr Ser Arg Ser Arg Ser Arg Ser Pro Gly
 580 585 590
 Ser Arg Ser Ser Ser Arg Ser Cys Tyr Tyr Tyr Glu Ser Ser His Tyr
 595 600 605

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Arg His Arg Thr His Arg Asn Ser Pro Leu Tyr Val Arg Ser Arg Ser
 610 615 620
 Arg Ser Pro Tyr Ser Arg Arg Pro Arg Tyr Asp Ser Tyr Glu Glu Tyr
 625 630 635 640
 Gln His Glu Arg Leu Lys Arg Glu Glu Tyr Arg Arg Glu Tyr Glu Lys
 645 650 655
 Arg Glu Ser Glu Arg Ala Lys Gln Arg Glu Arg Gln Arg Gln Lys Ala
 660 665 670
 Ile Glu Glu Arg Arg Val Ile Tyr Val Gly Lys Ile Arg Pro Asp Thr
 675 680 685
 Thr Arg Thr Glu Leu Arg Asp Arg Phe Glu Val Phe Gly Glu Ile Glu
 690 695 700
 Glu Cys Thr Val Asn Leu Arg Asp Asp Gly Asp Ser Tyr Gly Phe Ile
 705 710 715 720
 Thr Tyr Arg Tyr Thr Cys Asp Ala Phe Ala Ala Leu Glu Asn Gly Tyr
 725 730 735
 Thr Leu Arg Arg Ser Asn Glu Thr Asp Phe Glu Leu Tyr Phe Cys Gly
 740 745 750
 Arg Lys Gln Phe Phe Lys Ser Asn Tyr Ala Asp Leu Asp Ser Asn Ser
 755 760 765
 Asp Asp Phe Asp Pro Ala Ser Thr Lys Ser Lys Tyr Asp Ser Leu Asp
 770 775 780
 Phe Asp Ser Leu Leu Lys Glu Ala Gln Arg Ser Leu Arg Arg
 785 790 795